

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 076518-0150

re patent application of
JEFFERSON, RICHARD et al.

Serial No. 09/936,759

Filed: September 17, 2000

For: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

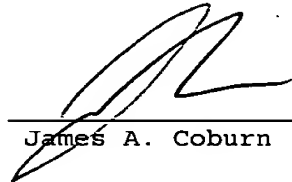
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/936,759

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

April 17, 2002
Date


James A. Coburn

HARBOR CONSULTING
Intellectual Property Services
1500A Lafayette Road
Suite 262
Portsmouth, N.H.
800-318-3021



SEQUENCE LISTING

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MAYER, JORGE E.

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USES THEREOF

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<141> 2000-09-17

<150> PCT/US00/07107

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<151> 1998-09-08

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 Gly Val Trp Asn Phe Lys Leu Asp Tyr Gly Lys Gly Leu Glu Glu Lys
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 Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser Met Ala Val Pro Ser
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 Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile Arg Asn His Ile Gly
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 Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu Lys Asp
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 Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr His Lys Ala Ile Val
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 Tyr Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro
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Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser Thr Leu Pro Val Gly	
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cta tat agt gaa aga cat gaa gaa ggt ttg gga aaa gtg att cgt aat	480
Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly Lys Val Ile Arg Asn	
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Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val	
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Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser Val Val	
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Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr Tyr Thr Val Asp Phe	
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Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val Val Asp Glu Glu Gly	
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Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr Leu Tyr Gln Ile Lys	
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Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg Glu Gly Leu Val Val	
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Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser Thr Trp Glu Lys Ile	
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Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Ala	
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Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe Lys Pro Leu Val Glu	
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Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro Val Thr Ile Val Leu	
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Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val Ala Glu Leu Ile Asp	
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Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr Glu Tyr Gly Ala Asp	
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Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe Ala Asp Phe Ala Thr	
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Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp Gly Met Asn Arg Val
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 275 280 285
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 305 310 315 320
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 325 330 335
 Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg Glu Gly Leu Val Val
 340 345 350
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545 550 555 560

Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys Lys Gly Val Phe Thr
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<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (1535)..(1536)

<223> a, c, t, g, other or unknown

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<221> modified_base

<222> (1551)..(1552)

<223> a, c, t, g, other or unknown

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<221> modified_base

<222> (1557)

<223> a, c, t, g, other or unknown

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<222> (1571)..(1572)

<223> a, c, t, g, other or unknown

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<221> modified_base

<222> (1593)

<223> a, c, t, g, other or unknown

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<221> modified_base

<222> (1605)

<223> a, c, t, g, other or unknown

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<221> modified_base

<222> (1609)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (1688)

<223> a, c, t, g, other or unknown

<400> 12

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ttgctgaccg aactatcacg actggctcgtg ctaagttgga ccacacattn cctgacaggg 180
gaaanacccg ccatatccat cttgtggccc aacagttagt taaccgtgtc gancctatat 240
ganggatcac tgnattcgag ctccntctta tgttcttcgc taacatanca tgnngtcata 300
tgtcaatang tgacnctggn cgtggatcac accgggctna ttgntgnatt cgaatttatg 360
tcaacaactt gttgcangnt ggatgaattg gtnacagggg ctttggccan catcctatac 420
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ttagtcgatg tggtttgtct nnnnagnnnn tanggttggg atncacaatc aggtgattta 1440
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aagccaatna tgtttacaga gtatggtgtg gatanngttg taggtttaca nncgatncc 1560
gataaaatgc nncagaaga gtataaaatg agnttttata aaggntatna taaaattatg 1620
gataaacgat cgcagctgag tacacgagct caccgcgga gtcgacaaga tccaagtact 1680
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<210> 13

<211> 628

<212> DNA

<213> Staphylococcus hominis

<220>

<221> modified_base

<222> (7)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (20)

<223> a, c, t, g, other or unknown

<400> 13

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tcctcagtcg ccgcctcggt ggcatgctc cacatcacga cgcttggatg gttcttgtca 120
cgagacacca gttcacggag aacgtcttga tgggtctcaa acgtccgaat cttctcccag 180
gtactgacgc gctcgtgccc ttccgccagt cccgtgggtg ccatgaagtt gaggtgcacg 240
ccaactgccg gagtctcgtc gatcacgacc agaccctcgc gatccgcaag acgcatcaac 300
ttctcagagt acggatagtg tgcggtccgg aagctgttgg cgccgatcca tttagggata 360
ttgaaatcca tcacattgct cgcttcgtta aagccacggc cgttgatagg agtgctccta 420
tgtttgccaa agcccttgaa gtagaacggt ttgttgttga tgaggaaact gccgtcgttg 480
acttcacggg ccgcacgccg aacggctctt catagacatc gatggtcaag tcccgtcgtt 540
caccagttcc actttgatct ggtagagata cgtgttcaag tggttcccag aggatgacat 600
tcggaatctt cacgttaccg ctcaagcc

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<210> 14
 <211> 1689
 <212> DNA
 <213> *Thermotoga maritima*

<220>
 <221> modified_base
 <222> (181)
 <223> a, c, t, g, other or unknown

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 caggatctgt gctacgaaga aggacccttc acctacaaaa ccaccttcta cgttccgaag 180
 naactttcac aaaaacacat cagactttac tttgctgctg tgaacacgga ctgagaggtc 240
 ttcctcaacg gagagaaagt gggagagaat cacattgaat accttcctt cgaagtagat 300
 gtgacgggga aagtgaatc cggagagaa gaactcaggg tgggtgttga gaacagattg 360
 aaagtgggag gatttccttc gaagggtcca gacagcggca ctcacaccgt gggatttttt 420
 ggaagttttc cacctgcaaa cttcgacttc tccccctacg gtggaatcat aaggcctgtt 480
 ctgatagagt tcacagacca cgcgaggata ctgcacatct ggggtggacac gagttagtct 540
 gaaccggaga agaaacttgg aaaagtgaag gtgaagatag aagtctcaga agaagcgggtg 600
 ggacaggaga tgacgatcaa acttgagag gaagagaaaa agattagaac atccaacaga 660
 ttctgcgaag gggagttcat cctcgaaaac gccaggttct ggagcctcga agatccatat 720
 ctttatcttc tcaaggtgga acttgaaaaa gacgagtaca ctctggacat cggaatcaga 780
 acgatcagct gggacgagaa gaggtcttat ctgaacggga aacctgtctt tttgaagggc 840
 tttggaaagc acgaggaatt ccccgttctg gggcagggca ccttttatcc attgatgata 900
 aaagacttca accttctgaa gtggatcaac gcgaattctt tcaggacctc tactatcct 960
 tacagtgaag agtggctgga tcttgccgac agactcggaa tccttgatgat agacgaagcc 1020
 ccgcacgttg gtatcacaag gtaccactac aatcccgaga ctcaagaagat agcagaagac 1080
 aacataagaa gaatgatcga cagacacaag aacctcccca gtgtgatcat gtggagtgtg 1140
 gcgaacgaac cagagtccaa ccatccagac gccggagggt tcttcaaagc ctttatgag 1200
 actgccaatg aaatggatcg aacacgcccc gttgtcatgg tgagcatgat ggacgcacca 1260
 gacgagagaa caagagacgt ggcgctgaag tacttcgaca tcgtctgtgt gaacaggtac 1320
 tacggctggt acatctatca gggaaggata gaagaaggac ttcaagctct ggaaaaagac 1380
 atagaagagc tctatgcaag gcacagaaag cccatctttg tcacagaatt cgggtcggac 1440
 gcgatagctg gcatccacta cgatccacct caaatgttct ccgaagagta ccaagcagag 1500
 ctctgtgaaa agacgatcag gctccttttg aaaaaagact acatcatcgg aacacacgtg 1560
 tgggcctttg cagattttta gactcctcag aatgtgagaa gacccattct caaccacaag 1620
 ggtgttttca caagagacag acaacccaaa ctctgtgctc atgtactgag aagactgtgg 1680
 agtgaggtt 1689

<210> 15
 <211> 602
 <212> PRT
 <213> *Staphylococcus* sp.

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 Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser Met Ala Val Pro Ser
 35 40 45

Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile Arg Asn His Ile Gly
 50 55 60
 Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu Lys Asp
 65 70 75 80
 Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr His Lys Ala Ile Val
 85 90 95
 Tyr Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro
 100 105 110
 Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp Gly Met Asn Arg Val
 115 120 125
 Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser Thr Leu Pro Val Gly
 130 135 140
 Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly Lys Val Ile Arg Asn
 145 150 155 160
 Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val
 165 170 175
 Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser Val Val
 180 185 190
 Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr Tyr Thr Val Asp Phe
 195 200 205
 Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val Val Asp Glu Glu Gly
 210 215 220
 Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly Asn Val Glu Ile Pro
 225 230 235 240
 Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr Leu Tyr Gln Ile Lys
 245 250 255
 Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp Val Tyr Glu Glu Pro
 260 265 270
 Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly Lys Phe Leu Ile Asn
 275 280 285
 Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys His Glu Asp Thr Pro
 290 295 300
 Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn Val Met Asp Phe Asn
 305 310 315 320
 Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg Thr Ala His Tyr Pro
 325 330 335
 Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg Glu Gly Leu Val Val
 340 345 350

Ile Asp Glu Thr Pro Ala Val Gly Val His Leu Asn Phe Met Ala Thr
 355 360 365
 Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser Thr Trp Glu Lys Ile
 370 375 380
 Arg Thr Phe Glu His His Gln Asp Val Leu Arg Glu Leu Val Ser Arg
 385 390 395 400
 Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Ala
 405 410 415
 Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe Lys Pro Leu Val Glu
 420 425 430
 Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro Val Thr Ile Val Leu
 435 440 445
 Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val Ala Glu Leu Ile Asp
 450 455 460
 Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr Phe Asp Gly Gly Asp
 465 470 475 480
 Leu Glu Ala Ala Lys Val His Leu Arg Gln Glu Phe His Ala Trp Asn
 485 490 495
 Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr Glu Tyr Gly Ala Asp
 500 505 510
 Thr Val Ala Gly Phe His Asp Ile Asp Pro Val Met Phe Thr Glu Glu
 515 520 525
 Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val Val Phe Asp Glu Phe
 530 535 540
 Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe Ala Asp Phe Ala Thr
 545 550 555 560
 Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys Lys Gly Val Phe Thr
 565 570 575
 Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val Phe Arg Glu Arg Trp
 580 585 590
 Thr Asn Ile Pro Asp Phe Gly Tyr Lys Asn
 595 600

<210> 16

<211> 613

<212> PRT

<213> Homo sapiens

<400> 16

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 Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro Leu
 35 40 45
 Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe Asn
 50 55 60
 Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val Trp
 65 70 75 80
 Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu Arg
 85 90 95
 Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile Val
 100 105 110
 Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu Pro
 115 120 125
 Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro Ser
 130 135 140
 Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr Thr
 145 150 155 160
 Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro
 165 170 175
 Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala
 180 185 190
 Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile
 195 200 205
 Asp Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val
 210 215 220
 Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val
 225 230 235 240
 Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr
 245 250 255
 Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr Leu
 260 265 270
 Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu Thr
 275 280 285
 Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro Val
 290 295 300
 Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn Gly
 305 310 315 320
 Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp Ile

	325		330		335
Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn Leu	340		345		350
Leu Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro Tyr	355		360		365
Ala Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val Ile	370		375		380
Asp Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn Asn	385		390		395
Val Ser Leu His His His Met Gln Val Met Glu Glu Val Val Arg Arg		405		410	415
Asp Lys Asn His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu Pro		420		425	430
Ala Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala		435		440	445
His Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn		450		455	460
Ser Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys		465		470	475
Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu		485		490	495
Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys Tyr		500		505	510
Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile Ala Gly		515		520	525
Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln Lys Ser		530		535	540
Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg Lys Tyr		545		550	555
Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr Glu Gln		565		570	575
Ser Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr Arg Gln		580		585	590
Arg Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg Tyr Trp Lys		595		600	605
Ile Ala Asn Glu Thr		610			

<211> 603
 <212> PRT
 <213> Escherichia coli

<400> 17

Met	Leu	Arg	Pro	Val	Glu	Thr	Pro	Thr	Arg	Glu	Ile	Lys	Lys	Leu	Asp	1	5	10	15
Gly	Leu	Trp	Ala	Phe	Ser	Leu	Asp	Arg	Glu	Asn	Cys	Gly	Ile	Asp	Gln	20	25	30	
Arg	Trp	Trp	Glu	Ser	Ala	Leu	Gln	Glu	Ser	Arg	Ala	Ile	Ala	Val	Pro	35	40	45	
Gly	Ser	Phe	Asn	Asp	Gln	Phe	Ala	Asp	Ala	Asp	Ile	Arg	Asn	Tyr	Ala	50	55	60	
Gly	Asn	Val	Trp	Tyr	Gln	Arg	Glu	Val	Phe	Ile	Pro	Lys	Gly	Trp	Ala	65	70	75	80
Gly	Gln	Arg	Ile	Val	Leu	Arg	Phe	Asp	Ala	Val	Thr	His	Tyr	Gly	Lys	85	90	95	
Val	Trp	Val	Asn	Asn	Gln	Glu	Val	Met	Glu	His	Gln	Gly	Gly	Tyr	Thr	100	105	110	
Pro	Phe	Glu	Ala	Asp	Val	Thr	Pro	Tyr	Val	Ile	Ala	Gly	Lys	Ser	Val	115	120	125	
Arg	Ile	Thr	Val	Cys	Val	Asn	Asn	Glu	Leu	Asn	Trp	Gln	Thr	Ile	Pro	130	135	140	
Pro	Gly	Met	Val	Ile	Thr	Asp	Glu	Asn	Gly	Lys	Lys	Lys	Gln	Ser	Tyr	145	150	155	160
Phe	His	Asp	Phe	Phe	Asn	Tyr	Ala	Gly	Ile	His	Arg	Ser	Val	Met	Leu	165	170	175	
Tyr	Thr	Thr	Pro	Asn	Thr	Trp	Val	Asp	Asp	Ile	Thr	Val	Val	Thr	His	180	185	190	
Val	Ala	Gln	Asp	Cys	Asn	His	Ala	Ser	Val	Asp	Trp	Gln	Val	Val	Ala	195	200	205	
Asn	Gly	Asp	Val	Ser	Val	Glu	Leu	Arg	Asp	Ala	Asp	Gln	Gln	Val	Val	210	215	220	
Ala	Thr	Gly	Gln	Gly	Thr	Ser	Gly	Thr	Leu	Gln	Val	Val	Asn	Pro	His	225	230	235	240
Leu	Trp	Gln	Pro	Gly	Glu	Gly	Tyr	Leu	Tyr	Glu	Leu	Cys	Val	Thr	Ala	245	250	255	
Lys	Ser	Gln	Thr	Glu	Cys	Asp	Ile	Tyr	Pro	Leu	Arg	Val	Gly	Ile	Arg	260	265	270	
Ser	Val	Ala	Val	Lys	Gly	Glu	Gln	Phe	Leu	Ile	Asn	His	Lys	Pro	Phe	275	280	285	

Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys
 290 295 300
 Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp
 305 310 315 320
 Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu
 325 330 335
 Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu Thr
 340 345 350
 Ala Ala Val Gly Phe Asn Leu Ser Leu Gly Ile Gly Phe Glu Ala Gly
 355 360 365
 Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu Thr
 370 375 380
 Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys
 385 390 395 400
 Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr
 405 410 415
 Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala Thr
 420 425 430
 Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe
 435 440 445
 Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu Cys
 450 455 460
 Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Thr
 465 470 475 480
 Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu
 485 490 495
 His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly
 500 505 510
 Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala
 515 520 525
 Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val
 530 535 540
 Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile
 545 550 555 560
 Leu Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys
 565 570 575
 Pro Lys Ser Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly Met Asn
 580 585 590

Phe Gly Glu Lys Pro Gln Gln Gly Gly Lys Gln
595 600

<210> 18

<211> 607

<212> PRT

<213> Staphylococcus sp.

<400> 18

Met Val Asp Leu Thr Ser Leu Tyr Pro Ile Asn Thr Glu Thr Arg Gly
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Val Phe Asp Leu Asn Gly Val Trp Asn Phe Lys Leu Asp Tyr Gly Lys
20 25 30

Gly Leu Glu Glu Lys Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser
35 40 45

Met Ala Val Pro Ser Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile
50 55 60

Arg Asn His Ile Gly Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro
65 70 75 80

Ala Tyr Leu Lys Asp Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr
85 90 95

His Lys Ala Ile Val Tyr Val Asn Gly Glu Leu Val Val Glu His Lys
100 105 110

Gly Gly Phe Leu Pro Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp
115 120 125

Gly Met Asn Arg Val Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser
130 135 140

Thr Leu Pro Val Gly Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly
145 150 155 160

Lys Val Ile Arg Asn Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly
165 170 175

Leu His Arg Pro Val Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu
180 185 190

Asp Ile Ser Val Val Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr
195 200 205

Tyr Thr Val Asp Phe Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val
210 215 220

Val Asp Glu Glu Gly Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly
225 230 235 240

Asn Val Glu Ile Pro Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr
245 250 255

Leu Tyr Gln Ile Lys Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp
 260 265 270
 Val Tyr Glu Glu Pro Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly
 275 280 285
 Lys Phe Leu Ile Asn Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys
 290 295 300
 His Glu Asp Thr Pro Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn
 305 310 315 320
 Val Met Asp Phe Asn Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg
 325 330 335
 Thr Ala His Tyr Pro Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg
 340 345 350
 Glu Gly Leu Val Val Ile Asp Glu Thr Pro Ala Val Gly Val His Leu
 355 360 365
 Asn Phe Met Ala Thr Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser
 370 375 380
 Thr Trp Glu Lys Ile Arg Thr Phe Glu His His Gln Asp Val Leu Arg
 385 390 395 400
 Glu Leu Val Ser Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser
 405 410 415
 Ile Ala Asn Glu Ala Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe
 420 425 430
 Lys Pro Leu Val Glu Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro
 435 440 445
 Val Thr Ile Val Leu Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val
 450 455 460
 Ala Glu Leu Ile Asp Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr
 465 470 475 480
 Phe Asp Gly Gly Asp Leu Glu Ala Ala Lys Val His Leu Arg Gln Glu
 485 490 495
 Phe His Ala Trp Asn Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr
 500 505 510
 Glu Tyr Gly Ala Asp Thr Val Ala Gly Phe His Asp Ile Asp Pro Val
 515 520 525
 Met Phe Thr Glu Glu Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val
 530 535 540
 Val Phe Asp Glu Phe Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe
 545 550 555 560
 Ala Asp Phe Ala Thr Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys

565

570

575

Lys Gly Val Phe Thr Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val
 580 585 590

Phe Arg Glu Arg Trp Thr Asn Ile Pro Asp Phe Gly Tyr Lys Asn
 595 600 605

<210> 19

<211> 376

<212> PRT

<213> Staphylococcus hominis

<220>

<221> MOD_RES

<222> (209)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (351)

<223> Any amino acid

<400> 19

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Leu Asn Thr Tyr Leu Tyr Gln Ile Lys Val Glu Leu Val Asn Asp Gly
 20 25 30

Leu Thr Ile Asp Val Tyr Glu Glu Pro Phe Gly Val Arg Thr Val Glu
 35 40 45

Val Asn Asp Gly Lys Phe Leu Ile Asn Asn Lys Pro Phe Tyr Phe Lys
 50 55 60

Gly Phe Gly Lys His Glu Asp Thr Pro Ile Asn Gly Arg Gly Phe Asn
 65 70 75 80

Glu Ala Ser Asn Val Met Asp Phe Asn Ile Leu Lys Trp Ile Gly Ala
 85 90 95

Asn Ser Phe Arg Thr Ala His Tyr Pro Tyr Ser Glu Glu Leu Met Arg
 100 105 110

Leu Ala Asp Arg Glu Gly Leu Val Val Ile Asp Glu Thr Pro Ala Val
 115 120 125

Gly Val His Leu Asn Phe Met Ala Thr Thr Gly Leu Gly Glu Gly Ser
 130 135 140

Glu Arg Val Ser Thr Trp Glu Lys Ile Arg Thr Phe Glu His His Gln
 145 150 155 160

Asp Val Leu Arg Glu Leu Val Ser Arg Asp Lys Asn His Pro Ser Val
 165 170 175

Val Met Trp Ser Ile Ala Asn Glu Ala Ala Thr Glu Glu Glu Gly Ala
 180 185 190
 Tyr Glu Tyr Phe Lys Pro Leu Gly Gly Ala Ala Lys Glu Leu Asp Pro
 195 200 205
 Xaa Lys Arg Pro Val Thr Ile Val Leu Phe Val Met Ala Thr Pro Glu
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 Thr Asp Lys Val Ala Glu Leu Ile Asp Val Ile Ala Leu Asn Arg Tyr
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 Asn Gly Trp Tyr Phe Asp Gly Gly Asp Leu Glu Ala Ala Lys Val His
 245 250 255
 Leu Arg Gln Glu Phe His Ala Trp Asn Lys Arg Cys Pro Gly Lys Pro
 260 265 270
 Ile Met Ile Thr Glu Tyr Gly Ala Asp Thr Val Ala Gly Phe His Asp
 275 280 285
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 Ala Asn His Val Val Phe Asp Glu Phe Glu Asn Phe Val Gly Glu Gln
 305 310 315 320
 Ala Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Val Met Arg Val
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 Gln Gly Asn Lys Lys Gly Val Phe Thr Arg Asp Arg Lys Pro Xaa Leu
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 35 40 45
 Leu Ser Trp Thr Thr His Xaa Leu Thr Gly Glu Xaa Pro Ala Ile Ser
 50 55 60
 Ile Leu Trp Pro Asn Ser Glu Leu Thr Val Ser Xaa Leu Tyr Xaa Gly
 65 70 75 80
 Ser Leu Xaa Ser Ser Ser Xaa Leu Cys Ser Ser Leu Thr Xaa His Val
 85 90 95
 Val Ile Cys Gln Xaa Val Thr Leu Xaa Val Asp His Thr Gly Leu Ile
 100 105 110
 Xaa Xaa Phe Glu Phe Met Ser Thr Thr Cys Cys Xaa Xaa Asp Glu Leu
 115 120 125
 Val Thr Gly Thr Leu Ala Xaa Ile Leu Tyr His Xaa Ile Leu Pro His
 130 135 140

Gly	Leu	Tyr	Arg	Lys	Arg	His	Glu	Xaa	Gly	Leu	Gly	Lys	Xaa	Asn	Phe	145	150	155	160
Tyr	Xaa	Leu	His	Phe	Ala	Phe	Phe	Xaa	Tyr	Ala	Xaa	Leu	Xaa	Arg	Thr	165	170	175	
Val	Xaa	Met	Tyr	Xaa	Asn	Leu	Val	Arg	Xaa	Gln	Asp	Ile	Val	Val	Thr	180	185	190	
Xaa	His	Xaa	Xaa	Xaa	Thr	Val	Glu	Gln	Cys	Val	Xaa	Xaa	Asn	Lys	Ile	195	200	205	
Xaa	Ser	Val	Lys	Ile	Thr	Ile	Leu	Asp	Glu	Asn	Asp	His	Ala	Ile	Xaa	210	215	220	
Glu	Ser	Glu	Gly	Ala	Lys	Gly	Asn	Val	Thr	Ile	Gln	Asn	Pro	Ile	Leu	225	230	235	240
Trp	Gln	Pro	Leu	His	Ala	Tyr	Leu	Tyr	Asn	Met	Lys	Val	Glu	Leu	Leu	245	250	255	
Asn	Asp	Asn	Glu	Cys	Val	Asp	Val	Tyr	Thr	Glu	Arg	Phe	Gly	Ile	Arg	260	265	270	
Ser	Val	Glu	Val	Lys	Asp	Gly	Gln	Phe	Leu	Ile	Asn	Asp	Lys	Pro	Phe	275	280	285	
Tyr	Phe	Lys	Gly	Phe	Gly	Lys	His	Glu	Asp	Thr	Tyr	Asn	Gly	Arg	Gly	290	295	300	
Leu	Asn	Glu	Ser	Ala	Asn	Val	Met	Asp	Ile	Asn	Leu	Met	Lys	Trp	Ile	305	310	315	320
Gly	Ala	Asn	Ser	Phe	Arg	Thr	Ser	His	Tyr	Pro	Tyr	Ser	Glu	Glu	Met	325	330	335	
Met	Arg	Leu	Ala	Asp	Glu	Gln	Gly	Ile	Val	Val	Ile	Asp	Glu	Thr	Thr	340	345	350	
Xaa	Val	Gly	Ile	His	Leu	Asn	Phe	Met	Xaa	Thr	Leu	Gly	Gly	Ser	Xaa	355	360	365	
Ala	His	Asp	Thr	Trp	Xaa	Glu	Phe	Asp	Thr	Leu	Glu	Phe	His	Lys	Glu	370	375	380	
Val	Ile	Xaa	Asp	Leu	Ile	Xaa	Arg	Asp	Lys	Asn	His	Ala	Trp	Val	Val	385	390	395	400
Met	Trp	Xaa	Phe	Gly	Asn	Glu	Xaa	Gly	Xaa	Asn	Lys	Gly	Gly	Ala	Lys	405	410	415	
Ala	Xaa	Phe	Glu	Pro	Phe	Val	Asn	Leu	Ala	Gly	Glu	Lys	Asp	Xaa	Xaa	420	425	430	
Xaa	Xaa	Pro	Val	Thr	Ile	Val	Thr	Ile	Leu	Xaa	Ala	Xaa	Arg	Asn	Val	435	440	445	
Cys	Glu	Val	Xaa	Asp	Leu	Val	Asp	Val	Val	Cys	Leu	Xaa	Xaa	Xaa	Xaa				

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Gly Trp Tyr Xaa Gln Ser Gly Asp Leu Glu Gly Ala Lys Xaa Ala Leu				
465		470		475 480
Asp Lys Glu Xaa Xaa Glu Trp Trp Lys Xaa Gln Xaa Asn Lys Pro Xaa				
	485		490	495
Met Phe Thr Glu Tyr Gly Val Asp Xaa Val Val Gly Leu Xaa Xaa Xaa				
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Pro Asp Lys Met Xaa Pro Glu Glu Tyr Lys Met Xaa Phe Tyr Lys Gly				
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Tyr Xaa Lys Ile Met Asp Lys				
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35 40 45
Pro Phe Thr Tyr Lys Thr Thr Phe Tyr Val Pro Lys Xaa Leu Ser Gln
50 55 60
Lys His Ile Arg Leu Tyr Phe Ala Ala Val Asn Thr Asp Cys Glu Val
65 70 75 80
Phe Leu Asn Gly Glu Lys Val Gly Glu Asn His Ile Glu Tyr Leu Pro
85 90 95
Phe Glu Val Asp Val Thr Gly Lys Val Lys Ser Gly Glu Asn Glu Leu
100 105 110
Arg Val Val Val Glu Asn Arg Leu Lys Val Gly Gly Phe Pro Ser Lys
115 120 125
Val Pro Asp Ser Gly Thr His Thr Val Gly Phe Phe Gly Ser Phe Pro
130 135 140
Pro Ala Asn Phe Asp Phe Phe Pro Tyr Gly Gly Ile Ile Arg Pro Val
145 150 155 160

Leu Ile Glu Phe Thr Asp His Ala Arg Ile Leu Asp Ile Trp Val Asp
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 180 185 190
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 195 200 205
 Gly Glu Glu Glu Lys Lys Ile Arg Thr Ser Asn Arg Phe Val Glu Gly
 210 215 220
 Glu Phe Ile Leu Glu Asn Ala Arg Phe Trp Ser Leu Glu Asp Pro Tyr
 225 230 235 240
 Leu Tyr Pro Leu Lys Val Glu Leu Glu Lys Asp Glu Tyr Thr Leu Asp
 245 250 255
 Ile Gly Ile Arg Thr Ile Ser Trp Asp Glu Lys Arg Leu Tyr Leu Asn
 260 265 270
 Gly Lys Pro Val Phe Leu Lys Gly Phe Gly Lys His Glu Glu Phe Pro
 275 280 285
 Val Leu Gly Gln Gly Thr Phe Tyr Pro Leu Met Ile Lys Asp Phe Asn
 290 295 300
 Leu Leu Lys Trp Ile Asn Ala Asn Ser Phe Arg Thr Ser His Tyr Pro
 305 310 315 320
 Tyr Ser Glu Glu Trp Leu Asp Leu Ala Asp Arg Leu Gly Ile Leu Val
 325 330 335
 Ile Asp Glu Ala Pro His Val Gly Ile Thr Arg Tyr His Tyr Asn Pro
 340 345 350
 Glu Thr Gln Lys Ile Ala Glu Asp Asn Ile Arg Arg Met Ile Asp Arg
 355 360 365
 His Lys Asn His Pro Ser Val Ile Met Trp Ser Val Ala Asn Glu Pro
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 Glu Ser Asn His Pro Asp Ala Glu Gly Phe Phe Lys Ala Leu Tyr Glu
 385 390 395 400
 Thr Ala Asn Glu Met Asp Arg Thr Arg Pro Val Val Met Val Ser Met
 405 410 415
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Tyr Ala Arg His Arg Lys Pro Ile Phe Val Thr Glu Phe Gly Ala Asp
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Asp Tyr Ile Ile Gly Thr His Val Trp Ala Phe Ala Asp Phe Lys Thr
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Ser Glu Val

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35 40 45

Gln Ile Val Ala Gln Gly Leu Gly Ala Thr Gly Ile Phe Glu Leu Asp
50 55 60

Asn Pro His Leu Trp Glu Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Arg
65 70 75 80

Val Thr Cys Glu Ala Asn Gly Glu Cys Asp Glu Tyr Pro Val Arg Val
85 90 95

Gly Ile Arg Ser Ile Thr Xaa Lys Gly Glu Gln Phe Leu Ile Asn His
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 Lys Pro Phe Tyr Leu Thr Gly Phe Gly Arg His Glu Asp Ala Asp Phe
 115 120 125
 Arg Gly Lys Gly Phe Asp Pro Val Leu Met Val His Asp His Ala Leu
 130 135 140
 Met Asn Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr
 145 150 155 160
 Ala Glu Lys Met Leu Asp Trp Ala Asp Glu His Val Ile Val Val Ile
 165 170 175
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 180 185 190
 Phe Asp Ala Gly Glu Arg Pro Lys Glu Leu Tyr Ser Glu Glu Ala Ile
 195 200 205
 Asn Gly Glu Thr Ser Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu
 210 215 220
 Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Cys Trp Ser Ile Ala
 225 230 235 240
 Asn Glu Pro Asp Thr Arg Pro Asn Gly Ala Arg Glu Tyr Phe Ala Pro
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 Gly Asp Leu Glu Lys Ala Glu Gln Met Leu Glu Gln Glu Leu Leu Ala
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 325 330 335
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Arg	Trp	Trp	Glu	Ser	Ala	Leu	Gln	Glu	Ser	Arg	Ala	Ile	Ala	Val	Pro	35	40	45	
Gly	Ser	Phe	Asn	Asp	Gln	Phe	Ala	Asp	Ala	Asp	Ile	Arg	Asn	Tyr	Ala	50	55	60	
Gly	Asn	Val	Trp	Tyr	Gln	Arg	Glu	Val	Phe	Ile	Pro	Lys	Gly	Trp	Ala	65	70	75	80
Gly	Gln	Arg	Ile	Val	Leu	Arg	Phe	Asp	Ala	Val	Thr	His	Tyr	Gly	Lys	85	90	95	
Val	Trp	Val	Asn	Asn	Gln	Glu	Val	Met	Glu	His	Gln	Gly	Gly	Tyr	Thr	100	105	110	
Pro	Phe	Glu	Ala	Asp	Val	Thr	Pro	Tyr	Val	Ile	Ala	Gly	Lys	Ser	Val	115	120	125	
Arg	Ile	Thr	Val	Cys	Val	Asn	Asn	Glu	Leu	Asn	Trp	Gln	Thr	Ile	Pro	130	135	140	
Pro	Gly	Met	Val	Ile	Thr	Asp	Glu	Asn	Gly	Lys	Lys	Lys	Gln	Ser	Tyr	145	150	155	160
Phe	His	Asp	Phe	Phe	Asn	Tyr	Ala	Gly	Ile	His	Arg	Ser	Val	Met	Leu	165	170	175	
Tyr	Thr	Thr	Pro	Asn	Thr	Trp	Val	Asp	Asp	Ile	Thr	Val	Val	Thr	His	180	185	190	
Val	Ala	Gln	Asp	Cys	Asn	His	Ala	Ser	Val	Asp	Trp	Gln	Val	Val	Ala	195	200	205	
Asn	Gly	Asp	Val	Ser	Val	Glu	Leu	Arg	Asp	Ala	Asp	Gln	Gln	Val	Val	210	215	220	
Ala	Thr	Gly	Gln	Gly	Thr	Ser	Gly	Thr	Leu	Gln	Val	Val	Asn	Pro	His	225	230	235	240
Leu	Trp	Gln	Pro	Gly	Glu	Gly	Tyr	Leu	Tyr	Glu	Leu	Cys	Val	Thr	Ala	245	250	255	
Lys	Ser	Gln	Thr	Glu	Cys	Asp	Ile	Tyr	Pro	Leu	Arg	Val	Gly	Ile	Arg	260	265	270	
Ser	Val	Ala	Val	Lys	Gly	Glu	Gln	Phe	Leu	Ile	Asn	His	Lys	Pro	Phe	275	280	285	

Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys
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 Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp
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 465 470 475 480
 Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu
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 His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly
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 accaaggaaa tccgcaacca tatcggatat gtctggtacg aacgtgagtt cacggtgccg 240
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 aatggcccaa ccgggactgt gacctatacg gtggactttc aaggcaaagc cgagaccgtg 660
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Val Phe Asp Leu Asn Gly Val Trp Asn Phe Lys Leu Asp Tyr Gly Lys
 20 25 30

Gly Leu Glu Glu Lys Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser
 35 40 45

Met Ala Val Pro Ser Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile
 50 55 60

Arg Asn His Ile Gly Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro
 65 70 75 80

Ala Tyr Leu Lys Asp Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr
 85 90 95

His Lys Ala Ile Val Tyr Val Asn Gly Glu Leu Val Val Glu His Lys
 100 105 110

Gly Gly Phe Leu Pro Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp
 115 120 125
 Gly Met Asn Arg Val Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser
 130 135 140
 Thr Leu Pro Val Gly Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly
 145 150 155 160
 Lys Val Ile Arg Asn Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly
 165 170 175
 Leu His Arg Pro Val Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu
 180 185 190
 Asp Ile Ser Val Val Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr
 195 200 205
 Tyr Thr Val Asp Phe Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val
 210 215 220
 Val Asp Glu Glu Gly Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly
 225 230 235 240
 Asn Val Glu Ile Pro Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr
 245 250 255
 Leu Tyr Gln Ile Lys Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp
 260 265 270
 Val Tyr Glu Glu Pro Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly
 275 280 285
 Lys Phe Leu Ile Asn Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys
 290 295 300
 His Glu Asp Thr Pro Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn
 305 310 315 320
 Val Met Asp Phe Asn Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg
 325 330 335
 Thr Ala His Tyr Pro Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg
 340 345 350
 Glu Gly Leu Val Val Ile Asp Glu Thr Pro Ala Val Gly Val His Leu
 355 360 365
 Asn Phe Met Ala Thr Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser
 370 375 380
 Thr Trp Glu Lys Ile Arg Thr Phe Glu His His Gln Asp Val Leu Arg
 385 390 395 400
 Glu Leu Val Ser Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser
 405 410 415
 Ile Ala Asn Glu Ala Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe

420						425						430					
Lys	Pro	Leu	Val	Glu	Leu	Thr	Lys	Glu	Leu	Asp	Pro	Gln	Lys	Arg	Pro		
435						440						445					
Val	Thr	Ile	Val	Leu	Phe	Val	Met	Ala	Thr	Pro	Glu	Thr	Asp	Lys	Val		
450						455						460					
Ala	Glu	Leu	Ile	Asp	Val	Ile	Ala	Leu	Asn	Arg	Tyr	Asn	Gly	Trp	Tyr		
465						470						475					
Phe	Asp	Gly	Gly	Asp	Leu	Glu	Ala	Ala	Lys	Val	His	Leu	Arg	Gln	Glu		
						485						490					
Phe	His	Ala	Trp	Asn	Lys	Arg	Cys	Pro	Gly	Lys	Pro	Ile	Met	Ile	Thr		
						500						505					
Glu	Tyr	Gly	Ala	Asp	Thr	Val	Ala	Gly	Phe	His	Asp	Ile	Asp	Pro	Val		
						515						520					
Met	Phe	Thr	Glu	Glu	Tyr	Gln	Val	Glu	Tyr	Tyr	Gln	Ala	Asn	His	Val		
						530						535					
Val	Phe	Asp	Glu	Phe	Glu	Asn	Phe	Val	Gly	Glu	Gln	Ala	Trp	Asn	Phe		
						545						550					
Ala	Asp	Phe	Ala	Thr	Ser	Gln	Gly	Val	Met	Arg	Val	Gln	Gly	Asn	Lys		
						565						570					
Lys	Gly	Val	Phe	Thr	Arg	Asp	Arg	Lys	Pro	Lys	Leu	Ala	Ala	His	Val		
						580						585					
Phe	Arg	Glu	Arg	Trp	Thr	Asn	Ile	Pro	Asp	Phe	Gly	Tyr	Lys	Asn	Ala		
						595						600					
Ser	His	His	His	His	His	His	Val										
						610						615					

<210> 29

<211> 16

<212> PRT

<213> Bacillus sp.

<400> 29

Met	Leu	Ile	Ile	Thr	Cys	Asn	His	Leu	His	Leu	Lys	Arg	Ser	Ala	Ile
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<210> 30

<211> 4

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Illustrative peptide

<400> 30
Lys Asp Glu Leu
1

<210> 31
<211> 6
<212> PRT
<213> Escherichia coli

<400> 31
Asp Phe Phe Asn Tyr Ala
1 5

<210> 32
<211> 5
<212> PRT
<213> Escherichia coli

<400> 32
Trp Asn Phe Ala Asp
1 5

<210> 33
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ayttyttyaa ytaygc

16

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (7)
<223> inosine

<400> 34
gaartcngcr aarttoca

18

<210> 35
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
atcgcacgtc ccactac

17

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
cgtgcatag gagttagc

18

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
atttagaaca tctcattatc cc

22

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
tgagatgttc taaatgaatt agc

23

<210> 39
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
atcgtgaccg gacgctt

17

<210> 40
<211> 17

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
gcgcgtaatc ttccctgg

17

<210> 41
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
tagcgacctt cgctttcgg

19

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
atcatgttta cagagtatgg

20

<210> 43
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 43
ggaatattgc acaatgggcg c

21

<210> 44
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 44
gatctctacg catttcaccg cta

23

<210> 45
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
atggtaagac cgcaacg

17

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
taaaaaccat ggtaagaccg caacg

25

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
cctcactcca cagtcttctc

20

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
agaccgctag cctcactcca cagtcttctc

30

<210> 49
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
tttgactttt tcaactatgc ag

22

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
aattctgcat agttgaaaaa gtc

23

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 51
gtcgacccat ggtagatctg actagtctgt acccg

35

<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 52
gtcgacagga gtgctatcat gctgtaccg

30

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 53
gtcgacagga gtgctacat ggtgtaccg

30

<210> 54
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 54

gtcgacagga gtgctacat gtagatctg taccg

36

<210> 55

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 55

gtagccatc accatcacca tcacgtgtga attggtgacc g

41

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 56

Ser Ser His His His His His His Val

1

5

<210> 57

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 57

tcgacccatg gtagatctga ctagtctgta cccgatcaac accgagaccc gtggcgtctt 60
cgacctcaat ggcgtctgga 80

<210> 58

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 58
ggatttcctt ggtcacgcca atgtcattgt aactgcttgg gacggccata ctaatagtgt 60
cggtcagctt gctttcgtac 80

<210> 59
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 59
ccaagcagtt acaatgacat tggcgtgacc aaggaaatcc gcaaccatat cggatatgtc 60
tggtacgaac gtgagttcac 80

<210> 60
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 60
gcgagcagc atacgctgat ccttcagata ggccggcacc gtgaactcac gttcgtacca 60
gacatatccg atatggttgc 80

<210> 61
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 61
ggtgccggcc tatctgaagg atcagcgtat cgtgctccgc ttcggctctg caactcacia 60
agcaattgtc tatgtcaatg 80

<210> 62
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 62
aatggcagga atccgccctt gtgtccacg accagctcac cattgacata gacaattgct 60

ttgtgagttg cagagccgaa

80

<210> 63

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 63

gtgagctggt cgtggagcac aagggcggat tcctgccatt cgaagcggaa atcaacaact 60
cgctgcgtga tggcatgaat 80

<210> 64

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 64

gtacagcccc accggtaggg tgctatcgtc gaggatgttg tccacggcga cggtagcgcg 60
attcatgcca tcacgcagcg agttgttgat ttccgcttcg 100

<210> 65

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 65

cgcgtcaccg tcgccgtgga caacatcctc gacgatagca ccctaccggt ggggct 56

<210> 66

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 66

cacttctctt ccagtccttt cccgtagtcc agcttgaagt tccagacgcc attgaggctg 60
aagacgccac gggctctcgt 80

<210> 67
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 67
ttgatcgggt acagactagt cagatctacc atggg

35

<210> 68
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 68
acttcaagct ggactacggg aaaggactgg aagagaagtg gtacgaaagc aagctgaccg 60
acactattag tatggccgtc 80

<210> 69
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 69
gtacagcgag cgccacgaag agggcctcgg aaaagtcatt cgtaacaagc cgaacttcga 60
cttcttcaac tatgcaggcc 80

<210> 70
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 70
ctttgccttg aaagtcacc gtataggtca cagtcccggt tgggccattg aagtcgggtca 60
caaccgagat gtctcgacg 80

<210> 71
<211> 80
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 71

accgggactg tgacctatac ggtggacttt caaggcaaag ccgagaccgt gaaagtgtcg 60
gtcgtggatg aggaaggcaa 80

<210> 72

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 72

ctccacgtta ccgtcaggc cctcgggtgt tgcgaccact ttgccttctt catccacgac 60
cgacactttc acggtctcgg 80

<210> 73

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 73

agtggtcgca agcaccgagg gcctgagcgg taacgtggag attccgaatg tcacccctctg 60
ggaaccactg aacacgtatc 80

<210> 74

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 74

gtcagtcggt cgttcaccag ttccactttg atctggtaga gatacgtggt cagtgggttc 60
cagaggatga cattcggaat 80

<210> 75

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 75

tctaccagat caaagtggaa ctggtgaacg acggactgac catcgatgtc tatgaagagc 60
cgttcggcgt gcggaccgtg 80

<210> 76

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 76

acggtttgtt gttgatgagg aacttgccgt cgttgacttc cacggtcgcg acgccgaacg 60
gctcttcata gacatcgatg 80

<210> 77

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 77

gaagtcaacg acggcaagtt cctcatcaac aacaaaccgt tctacttcaa gggctttggc 60
aaacatgagg acactcctat 80

<210> 78

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 78

tacgtaaacg gggtcgtgta gattttcacc ggacggtgca ggcctgcata gttgaagaag 60
tcgaagttcg gcttgttacg 80

<210> 79

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 79

atccatcaca ttgctcgctt cgtaaagcc acggccgttg ataggagtgt cctcatgttt 60
 gccaaagccc ttgaagtaga. 80

<210> 80

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 80

caacggccgt ggctttaacg aagcgagcaa tgtgatggat ttcaatatcc tcaaattggat 60
 cggcgccaac agctt 75

<210> 81

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 81

aatgactttt ccgaggccct cttcgtggcg ctcgct 36

<210> 82

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 82

ccggaagctg ttggcgccga tccatttgag gatattgaa 39

<210> 83

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 83

tgcaccgtcc ggtgaaaatc tacacgaccc cgtttacgta cgtcgaggac atctcggttg 60

tgaccgactt caatggccca

80

<210> 84

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 84

ccggaccgca cactatccgt actctgaaga gttgatgcgt cttgcggatc gcgagggctc 60
ggtcgtgatc gacgagactc 80

<210> 85

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 85

gttcacggag aacgtcttga tgggtgctcaa acgtccgaat cttctcccag gtactgacgc 60
gctcgtgcc ttcgccgagt 80

<210> 86

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 86

attcggacgt ttgagcacca tcaagacgtt ctccgtgaac tgggtgtctcg tgacaagaac 60
catccaagcg tcgtgatgtg 80

<210> 87

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 87

cgcgcctct tctcagtcg ccgcctcgtt ggcgatgctc cacatcacga cgcttggatg 60
gttcttgtca cgagacacca 80

<210> 88
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 88
 gagcatcgcc aacgaggcgg cgactgagga agagggcgcg tacgagtact tcaagccgtt 60
 ggtggagctg accaaggaac 80

<210> 89
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 89
 acaaacagca cgatcgtgac cggacgcttc tgtgggtcga gttccttggt cagctccacc 60
 aacggcttga agtactcgta 80

<210> 90
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 90
 tcgaccacaca gaagcgctccg gtcacgatcg tgctgtttgt gatggctacc ccggagacgg 60
 acaaagtcgc cgaactgatt 80

<210> 91
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 91
 cgaagtacca tccgttatag cgattgagcg cgatgacgtc aatcagttcg gcgactttgt 60
 ccgtctccgg ggtagccatc 80

<210> 92

<211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 92
 gacgtcatcg cgctcaatcg ctataacgga tggctacttcg atggcgggtga tctcgaagcg 60
 gccaaagtcc atctccgcca ggaatttca 89

<210> 93
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 93
 cccgtggtgg ccatgaagtt gaggtgcacg ccaactgccg gagtctcgtc gatcacgacc 60
 agaccctcgc gatccgcaag 80

<210> 94
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 94
 cgcgtgaaat tcttggcgga gatggacttt ggccgcttcg agatcaccgc cat 53

<210> 95
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 95
 acgcatcaac tcttcagagt acggatagtg tgcggt 36

<210> 96
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 96

cggcagttgg cgtgcacctc aacttcattg ccaccacggg actcggcgaa ggcagcgagc 60
gcgtcagtac ctgggagaag 80

<210> 97

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 97

cgcgtggaac aagcgttgcc caggaaagcc gatcatgac actgagtagc gcgcagacac 60
cgttcggggc tttcacgaca 80

<210> 98

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 98

tcgcgaagtc cgcgaagttc cacgcttgct caccacgaa gttctcaaac tcacgaaca 60
cgacgtgggt cgcttgtag 80

<210> 99

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 99

ttcgtgggtg agcaagcgtg gaacttcgcg gacttcgca cctctcaggg cgtgatgcgc 60
gtccaaggaa acaagaaggg 80

<210> 100

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 100

gtgcgcggcg agcttcggct tgcggtcacg agtgaacacg cccttcttgt ttccttggac 60
 gcgcatcacg ccttgagagg 80

<210> 101

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 101

cgtgttcaact cgtgaccgca agccgaagct cgccgcgcac gtctttcgcg agcgctggac 60
 caacattcca gatttcggct 80

<210> 102

<211> 89

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 102

cggtcaccaa ttcacacgtg atggatgatgg tgatggctag cgttcttgta gccgaaatct 60
 ggaatgttgg tccagcgctc gcgaaagac 89

<210> 103

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 103

acaagaacgc tagccatcac catcaccatc acgtgtgaat tggtgaccgg gcc 53

<210> 104

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 104

tactcgactt gatattcctc ggtgaacatc actggatcaa tgcgtgaaa gcccgcaacg 60
gtgtctgcgc cgtactcagt 80

<210> 105
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 105
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<210> 106
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 106
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tgttcgatga gtttgagaac 80

<210> 107
<211> 60
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Invertase signal
sequence used in yeast vector

<400> 107
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<210> 108
<211> 258
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Mat alpha signal
sequence used in yeast vector

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tacttagatt tagaagggga tttcgatggt gctgttttgc cattttccaa cagcacaaat 180
aacgggttat tgtttataaa tactactatt gcccagcatt ctgctaaaga agaaggggta 240

tcttttgata aaagagag

258

<210> 109

<211> 88

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Extensin signal
sequence used in plant vector

<400> 109

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agcttctgaa agctcagcaa attatcaa 88

<210> 110

<211> 82

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: GRP signal
sequence used in plant vector

<400> 110

catggctact actaagcatt tggctcttgc catccttgtc ctccttagca ttggtatgac 60
caccagtgc agaaccctcc ta 82

<210> 111

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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<221> modified_base

<222> (26)..(27)

<223> a, c, t, g, other or unknown

<400> 111

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43

<210> 112

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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 <221> modified_base
 <222> (17)..(18)
 <223> a, c, t, g, other or unknown

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43

<210> 113
 <211> 1812
 <212> DNA
 <213> Salmonella sp.

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 caaagccgcg ctatcgccgt tccgggaagc tataacgac agtttgccgc tgccgagatc 180
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 gataaataat ga 1812

<210> 114
 <211> 602
 <212> PRT
 <213> Salmonella sp.

<400> 114
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Gly Leu Trp Ser Phe Cys Met Asp Ser Glu Glu Cys Gly Asn Ala Gln

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	35					40						45			
Gly	Ser	Tyr	Asn	Asp	Gln	Phe	Ala	Ala	Ala	Glu	Ile	Arg	Asn	Tyr	Val
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Gly	Asn	Val	Trp	Tyr	Gln	Arg	Glu	Ile	Arg	Ile	Pro	Lys	Gly	Trp	Asp
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Arg	Gln	Arg	Ile	Val	Leu	Arg	Phe	Asp	Ala	Val	Thr	His	Tyr	Gly	Lys
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Val	Trp	Val	Asn	Asp	Gln	Phe	Leu	Met	Glu	His	Gln	Gly	Gly	Tyr	Thr
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Pro	Phe	Glu	Ala	Asp	Ile	Ser	His	Leu	Ile	Ser	Ala	Gly	Glu	Ser	Val
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Phe	His	Asp	Phe	Phe	Asn	Tyr	Ala	Gly	Ile	His	Arg	Ser	Val	Met	Leu
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Tyr	Thr	Thr	Pro	Lys	Thr	Phe	Val	Glu	Asp	Ile	Thr	Val	Val	Thr	Gln
			180					185					190		
Val	Ala	Asp	Asp	Leu	Ala	Gln	Ala	Thr	Val	Ala	Trp	Gln	Val	Arg	Ala
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Leu	Trp	Gln	Pro	Gly	Glu	Gly	Tyr	Leu	Tyr	Glu	Leu	Arg	Val	Ile	Ala
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Gln	His	Gln	Asp	Glu	Gln	Asp	Glu	Tyr	Pro	Leu	Arg	Val	Gly	Ile	Arg
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Ser	Val	Glu	Val	Lys	Gly	Glu	Gln	Phe	Leu	Ile	Asn	His	Lys	Pro	Phe
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	290					295					300				
Gly	Phe	Asp	Asn	Val	Leu	Met	Val	His	Asp	His	Ala	Leu	Met	Asp	Trp
	305					310					315				320
Ile	Gly	Ala	Asn	Ser	Tyr	Arg	Thr	Ser	His	Tyr	Pro	Tyr	Ala	Glu	Glu
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Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Ile Ile Asp Glu Thr
 340 345 350
 Ala Ala Val Gly Phe Asn Leu Ser Leu Gly Ile Ser Phe Asp Val Gly
 355 360 365
 Glu Lys Pro Lys Glu Leu Tyr Ser Asp Glu Ala Val Asn Asp Glu Thr
 370 375 380
 Gln Arg Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys
 385 390 395 400
 Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr
 405 410 415
 Arg Pro Asn Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Gln Ala Thr
 420 425 430
 Arg Glu Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe
 435 440 445
 Cys Asp Ala Glu Ser Asp Thr Ile Thr Asp Leu Phe Asp Val Val Cys
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 Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Lys
 465 470 475 480
 Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu
 485 490 495
 His Arg Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly
 500 505 510
 Leu His Ser Met Tyr Asn Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala
 515 520 525
 Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val
 530 535 540
 Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile
 545 550 555 560
 Met Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys
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<210> 115

<211> 1822

<212> DNA

<213> Staphylococcus sp.

<400> 115

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<210> 116

<211> 1980

<212> DNA

<213> Escherichia coli

<400> 116

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<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6x His tag

<400> 117

His His His His His His

1

5

<210> 118

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 118

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17

<210> 119

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 119

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17

<210> 120

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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15